

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia

(ii) TITLE OF INVENTION: Ligands for flt3 Receptors

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Macintosh 7.0.1
(D) SOFTWARE: Microsoft Word, Version #5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: -to be assigned-
(B) FILING DATE: March 7, 1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/162,407
(B) FILING DATE: December 3, 1993
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/111,758
(B) FILING DATE: August 25, 1993
(C) CLASSIFICATION:

(ix) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/106,463
(B) FILING DATE: August 12, 1993
(C) CLASSIFICATION:

(x) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/068,394
(B) FILING DATE: May 24, 1993
(C) CLASSIFICATION:

(xi) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..25
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 855..879
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGCACTGGA	ACGAGACGAC	CTGCTCTGTC	ACAGGCATGA	GGGGTCCCCG	GCAGAG	56																										
ATG	ACA	GTG	CTG	GCG	CCA	TGG	AGC	CCA	AAT	TCC	TCC	CTG	TTG	CTG	Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Asn	Ser	Ser	Leu	Leu	Leu	104	
1					5					10																					15	
CTG	TTG	CTG	CTG	CTG	AGT	CCT	TGC	CTG	CGG	GGG	ACA	CCT	GAC	TGT	TAC	Leu	Leu	Leu	Leu	Ser	Pro	Cys	Leu	Arg	Gly	Thr	Pro	Asp	Cys	Tyr	152	
20						25																									30	
TTC	AGC	CAC	AGT	CCC	ATC	TCC	TCC	AAC	TTC	AAA	GTG	AAG	TTT	AGA	GAG	Phe	Ser	His	Ser	Pro	Ile	Ser	Ser	Asn	Phe	Lys	Val	Lys	Phe	Arg	Glu	200
35						40																									45	
TTG	ACT	GAC	CAC	CTG	CTT	AAA	GAT	TAC	CCA	GTC	ACT	GTG	GCC	GTC	AAT	Leu	Thr	Asp	His	Leu	Leu	Lys	Asp	Tyr	Pro	Val	Thr	Val	Ala	Val	Asn	248
50						55																									60	
CTT	CAG	GAC	GAG	AAG	CAC	TGC	AAG	GCC	TTG	TGG	AGC	CTC	TTC	CTA	GCC	Leu	Gln	Asp	Glu	Lys	His	Cys	Lys	Ala	Leu	Trp	Ser	Leu	Phe	Leu	Ala	296
65						70																									80	
CAG	CGC	TGG	ATA	GAG	CAA	CTG	AAG	ACT	GTG	GCA	GGG	TCT	AAG	ATG	CAA	Gln	Arg	Trp	Ile	Glu	Gln	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	344
85							90																								95	
ACG	CTT	CTG	GAG	GAC	GTC	AAC	ACC	GAG	ATA	CAT	TTT	GTC	ACC	TCA	TGT	Thr	Leu	Leu	Glu	Asp	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Ser	Cys	392
100							105																								110	
ACC	TTC	CAG	CCC	CTA	CCA	GAA	TGT	CTG	CGA	TTC	GTC	CAG	ACC	AAC	ATC	Thr	Phe	Gln	Pro	Leu	Pro	Glu	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	440
115							120																								125	
TCC	CAC	CTC	CTG	AAG	GAC	ACC	TGC	ACA	CAG	CTG	CTT	GCT	CTG	AAG	CCC	Ser	His	Leu	Leu	Lys	Asp	Thr	Cys	Thr	Gln	Leu	Leu	Ala	Leu	Lys	Pro	488
130							135																								140	

TGT ATC GGG AAG GCC TGC CAG AAT TTC TCT CGG TGC CTG GAG GTG CAG	536
Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln	
145 150 155 160	
TGC CAG CCG GAC TCC TCC ACC CTG CTG CCC CCA AGG AGT CCC ATA GCC	584
Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala	
165 170 175	
CTA GAA GCC ACG GAG CTC CCA GAG CCT CGG CCC AGG CAG CTG TTG CTC	632
Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu	
180 185 190	
CTG CTG CTG CTG CCT CTC ACA CTG GTG CTG CTG GCA GCC GCC TGG	680
Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp	
195 200 205	
GGC CTT CGC TGG CAA AGG GCA AGA AGG AGG GGG GAG CTC CAC CCT GGG	728
Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly	
210 215 220	
GTC CCC CTC CCC TCC CAT CCC TAGGATTGCA GCCTTGCA TCGTTGACTC	779
Val Pro Leu Pro Ser His Pro	
225 230	
AGCCAGGGTC TTATCTCGGT TACACCTGTA ATCTCAGCCC TTGGGAGCCC AGAGCAGGAT	839
TGCTGAATGG TCTGGAGCAG GTCGTCTCGT TCCAGTCGAC	879

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu	
1 5 10 15	
Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr	
20 25 30	
Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu	
35 40 45	
Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn	
50 55 60	
Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala	
65 70 75 80	
Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln	
85 90 95	
Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys	
100 105 110	
Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile	
115 120 125	

Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
130 135 140

Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
145 150 155 160

Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
165 170 175

Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
180 185 190

Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Ala Ala Ala Trp
195 200 205

Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
210 215 220

Val Pro Leu Pro Ser His Pro
225 230

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCAGGTCGT CTCGTTCCAG

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 988 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 30..734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCCGGAAT	TCCGGGGCCC	CCGGCCGAA	ATG	ACA	GTG	CTG	GCG	CCA	GCC	TGG	53
			Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	
			1				5				
AGC	CCA	ACA	ACC	TAT	CTC	CTC	CTG	CTG	CTG	CTG	101
Ser	Pro	Thr	Thr	Tyr	Leu	Leu	Leu	Leu	Leu	Ser	
10					15				20		
AGT	GGG	ACC	CAG	GAC	TGC	TCC	TTC	CAA	CAC	AGC	149
Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	
25					30			35		40	
TTC	GCT	GTC	AAA	ATC	CGT	GAG	CTG	TCT	GAC	TAC	197
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	
				45			50			55	
CCA	GTC	ACC	GTG	GCC	TCC	AAC	CTG	CAG	GAC	GAG	245
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	
				60			65			70	
CTC	TGG	CGG	CTG	GTC	CTG	GCA	CAG	CGC	TGG	ATG	293
Leu	Trp	Arg	Leu	Val	Ala	Gln	Arg	Trp	Met	Glu	
				75			80			85	
GTC	GCT	GGG	TCC	AAG	ATG	CAA	GGC	TTG	CTG	GAG	341
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	
				90			95			100	
ATA	CAC	TTT	GTC	ACC	AAA	TGT	GCC	TTT	CAG	CCC	389
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	
				105			110			115	
CGC	TTC	GTC	CAG	ACC	AAC	ATC	TCC	CGC	CTC	CTG	437
Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	
				125			130			135	
CAG	CTG	GTG	GCG	CTG	AAG	CCC	TGG	ATC	ACT	CGC	485
Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	
				140			145			150	
TGC	CTG	GAG	CTG	CAG	TGT	CAG	CCC	GAC	TCC	ACC	533
Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	
				155			160			165	
5	TGG	AGT	CCC	CGG	CCC	CTG	GAG	GCC	ACA	GCC	581
	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	Thr	Ala	
				170			175			180	
CCT	CTG	CTC	CTA	CTG	CTG	CCC	GTG	GGC	CTC	CTG	629
Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Val	Gly	Leu	
				185			190			195	
GCT	GCC	TGG	TGC	CTG	CAC	TGG	CAG	AGG	ACG	CGG	677
Ala	Ala	Trp	Cys	Leu	His	Trp	Gln	Arg	Thr	Arg	
				205			210			215	

CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT	725
Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu	
220 225 230	
GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC	774
Val Glu His	
235	
GCAGTGAGAC AGACATCTAT CATCCCATT TACAGGGGAG GATACTGAGG CACACAGAGG	834
GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC	894
CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC	954
GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG	988

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu	
1 5 10 15	
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe	
20 25 30	
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu	
35 40 45	
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu	
50 55 60	
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln	
65 70 75 80	
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly	
85 90 95	
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala	
100 105 110	
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser	
115 120 125	
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp	
130 135 140	
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro	
145 150 155 160	
Asp Ser Ser Thr Leu Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala	
165 170 175	
Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu	
180 185 190	
Pro Val Gly Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln	
195 200 205	

Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val
210 215 220

Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His
225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT 60

ACTTCAGCCA C 71

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

37